

# Modular evolution and complexity increase in replicating RNA populations

Susanna C. Manrubia

*Transdisciplinary Laboratory*

*Centro de Astrobiología (CSIC-INTA)*

*Carretera de Ajalvir, Km. 4. 28850 Torrejón de Ardoz. Madrid*

*SPAIN*

[cuevasms@inta.es](mailto:cuevasms@inta.es)

Carlos Briones

*Molecular Evolution Laboratory*

*Centro de Astrobiología (CSIC-INTA)*

*Carretera de Ajalvir, Km. 4. 28850 Torrejón de Ardoz. Madrid*

*SPAIN*

The first stages of molecular evolution required a rapid increase in molecular complexity in order to guarantee a structural/functional repertory of variants. This likely necessitated evolutionary processes additional to the accumulation of advantageous mutations, such as the shuffling of molecular modules or motifs.

We study the evolution of two randomly generated identical populations,  $A$  and  $B$ , of 35 nucleotides (nt) long, single stranded (ss) RNA sequences. In this first numerical experiment, each population consists of  $N$  sequences that evolve independently, at discrete generations and subject to a high mutation rate, with the goal of reaching a prefixed secondary structure (motifs  $S_A$  and  $S_B$ , respectively). Once this objective is achieved, we analyze the sequence diversity within the final populations and the coexisting secondary structures. In a second step, the two populations are combined to produce 70-nt long sequences. The resulting sequences are folded and the ensemble of secondary structures produced is compared with the original ones. Our objective is to identify sequences in the population  $AB$  that contain both motifs  $S_A$  and  $S_B$  (in a combined structure  $S_{AB}$ ). In a second experiment, a population  $C$  of  $N$  70-nt long ssRNA sequences evolves towards the prefixed goal structure  $S_{AB}$ . We analyze the final population in the sequence and the structure space, and compare the time needed to reach  $S_{AB}$  in the first and in the second experiment.

This allows us to discuss the relevance of independent modular evolution of functional motifs in the increase of molecular complexity, in the RNA world context.